Seq140-aay87247.res

PARAMETERS

infarity matrix PAM-150 K-tuple 1

ireshold level of sim. 16% Joining penalty 20 smatch penalty 5.00 Window size 1

ip penalty 0.05 Itoff score 1 indomization group 0

SEARCH STATISTICS

ne scores below are sorted by initial score. ignificance is calculated based on initial score.

100% identical sequence to the query sequence was not found.

ne list of best scores is:

Frame	0							
F	! ! 0		0 11 1	70 FYKTW FYKTW 70	GLY GLY GLY	<u>}</u> _}	PLSP PLSP	
Sig.	0.0		0.00	70 TFYKTW FYKTW 70	140 Libsgly Libsgly 140	3-3	6 — 6 5 — 6	
S				>>	75-57	210 LCLPLI 	й—й ж—в	
ig.	310	E S		60 PVDKGHDV PVDKGHDV 60	ITMRNLT] TMRNLT]		280 GRHLLSE GRHLLSE 280	
Opt. Score		4	anc es	60 GPVDKGHD' GPVDKGHD' GPVDKGHD'	# H H L	NGI H	3GE	
rt Re	310	P-2	fic	CRLLG 	130 130 130		SES SES	
Init. Score	3	HSP	Significance Mismatches	TCRLL 		200 LATGACIV	270 0RQF 270	
th	311	protein HSPP-		50 CPEGONVTLT CPEGONVTLT 50	120 ORHGLESASDHHGNFSI ORHGLESASDHHGNFSI 120	<u> </u>	270 rvaorops: rvaorops	
Length	3.	ote	310 309 ions	SO CPEGONVTI CPEGONVTI	120 GLES GLES 120	4 — H		
			3 uti	CPE CPE CPE	RHG HHG	190 SEN SEN 190	260 KVRHPI KVRHPI 260	
	containi	containing	re = 310 = 309 Substitutions	SLYV SLYV	5=5	SSODSENIT SSOESENIT 190	260 AKVRI AKVRI 260	
	ont	ain	e ubs	TPYSI TPYSI TPYSI 40	SHD SHD SHD	S — S	HEA HEA HEA	
		ont	0	FKVAT FKVAT	110 ANTSI ANTSI 110	180 CVVYPS CVVYPS	8—8 —8 —8	
	tid			30 PVAAFKVATPY PVAAFKVATPY 30	СНОР 	180 PSNCVVY PSNCVVX	250 	
	peptide	peptide	Optimized Sco Matches Conservative	30 GPVAA GPVAA 30	100 HILHGGHQAANTSHDI HILHGGHQAANTSHDI 100	160 170 EHXYHGAMELQVQTGKDAPSN EHXYHGAMELQVQTGKDAPSN 160	230 240 280 280 280 280 261 261 261 261 261 261 261 261 261 261	
		pep	Optimiz Matches Conserv	JJ	100 ODLHLHHG ODLHLHHG	150 CCLVVETRHHHSEHRYHGAMELOVOTGKDA 	04 X	
Description	signal	11)	O K O	LAAS:	8-8	170 0V0T 0V0T 170	240 OGIE OGIE 240	×H-H-
ipt		1-3 ign	310 998 0	20 FALFL FALFL 20	17—17 17—18 17—18	MET.	SNIO	X FEVI FEVI 310
BCI	Нишап) ©	w ou	남그님	90 PIRNI PIRNI 90	HGA HGA	MDS MDS	NG S HNG S ING S
Ö	<u> </u>	-14 uma	0 11 18	wgs wgs	90 CSERRPIRNLTF SERRPIRNLTF 90	160 HRVJ HRVJ 160	011-110 R-110	7 – 7 1 – 7 1 – 7
	!	-485A-140 (1-311) Human signal	tγ	X MGVPTALEAGSWRWGS MGVPTAPEAGSWRWGS X	ESSE 	HSE HSE	230 RAQELVRMD RAQELVRMD 230	300 PSLDPVPDSPNFEVI PSLDPVPDSPNFEVI 300
e e	aay87247	6-4	·H	EAG EAG	80 EVOT 	150 CLVVEIRHHHS CLVVEIRHHHS 150	220 KORQAASNRRA KORQAASNRRA 220	[14 [14
Name	y87	US-10-006-	Score	TAL TAP	RGEV RGEV BGEV	150 VVEI VVEI 150	220 KORQAASNR KORQAASNR 220	O GPGDVF GPGDVF O
nce	aa	787	g al	GVP 	YRSSRG YRSSRG	15=61	20-020 20-030 200-000	90 PGPGDV PGPGDV 909
Sequence	ļ÷	a a	Initial Residue Gaps	׎—Ž×	≯ >+	ŏŏ	x-x	290 - 290 - 290 - 290
S	!	i,	G Re G					